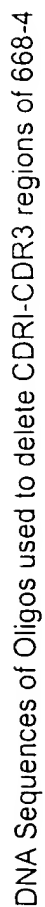


FIG. 1



Kappa Chain

Framework 4

Stop Stop Stop Framework 1

TAT TTC CAG CTT GGT CCC TCT AGA GTT AAC GAT ATC AA CGT TTA T CTA A TCA GCA AGA GAT GGA GGC TTG

Heavy Chain

Framework 4

Stop Stop Stop Framework 4

TTG GGT TCC TTG ACC CCA CTG CAG AGT ACT AGG CCT CT GAG CTA C TCA G TTA GGT GAT TGA GTA GCC AGT

FIG. 2

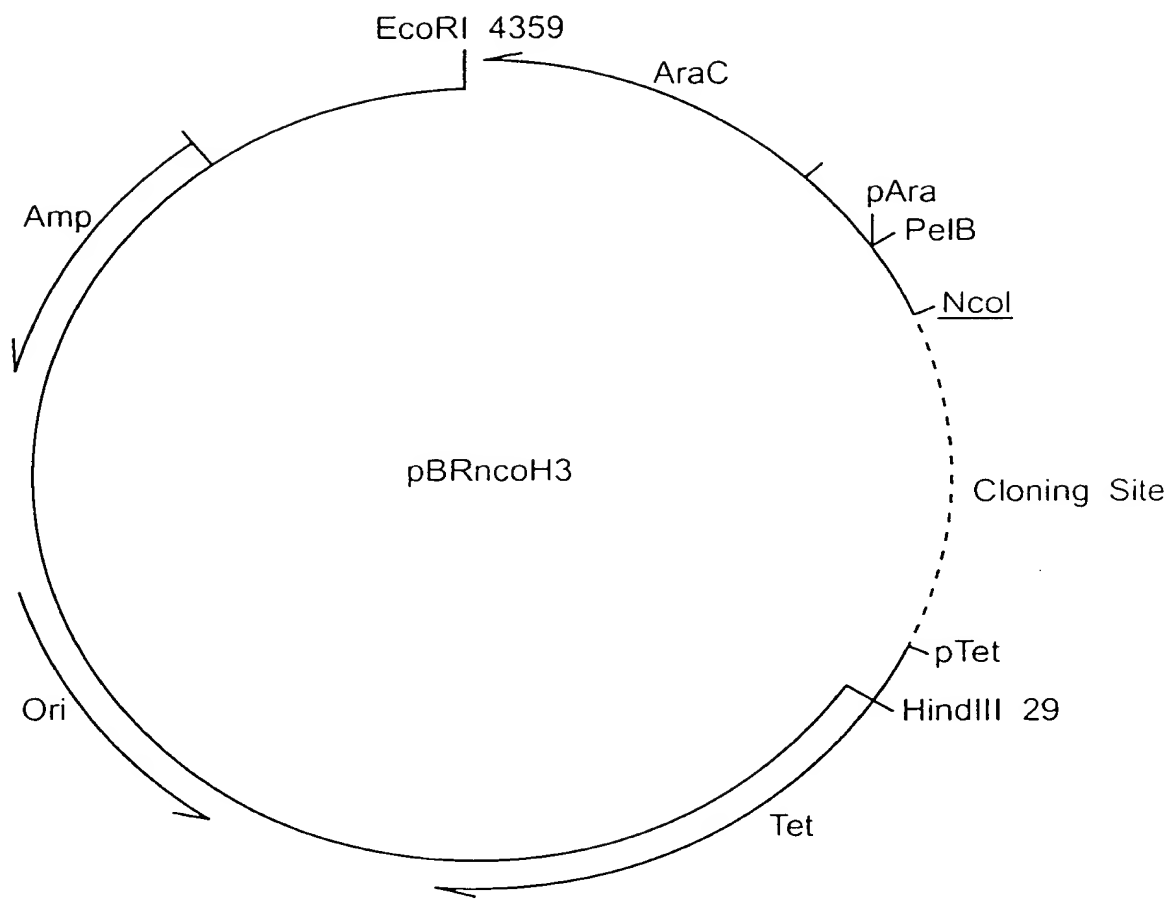


FIG. 3

AraCpBAD insert as subcloned into 14F8 to generate the pBRncoH3 cloning vector

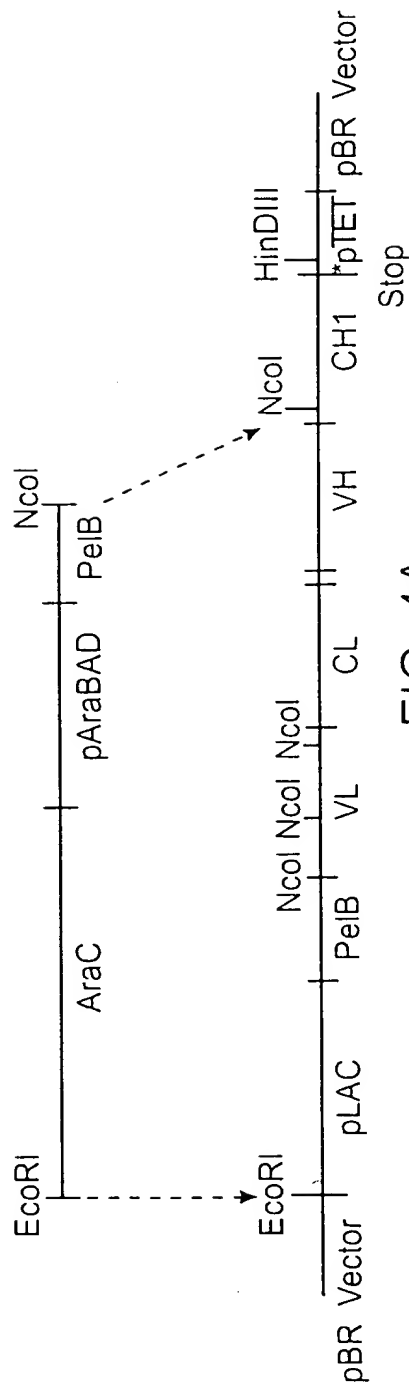
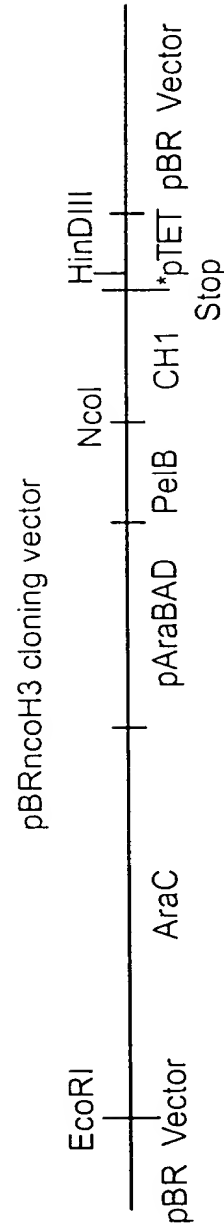


FIG. 4A



* represents 19 base pairs at the 5' -end of the tetracycline promoter removed by HindIII digestion

FIG. 4B

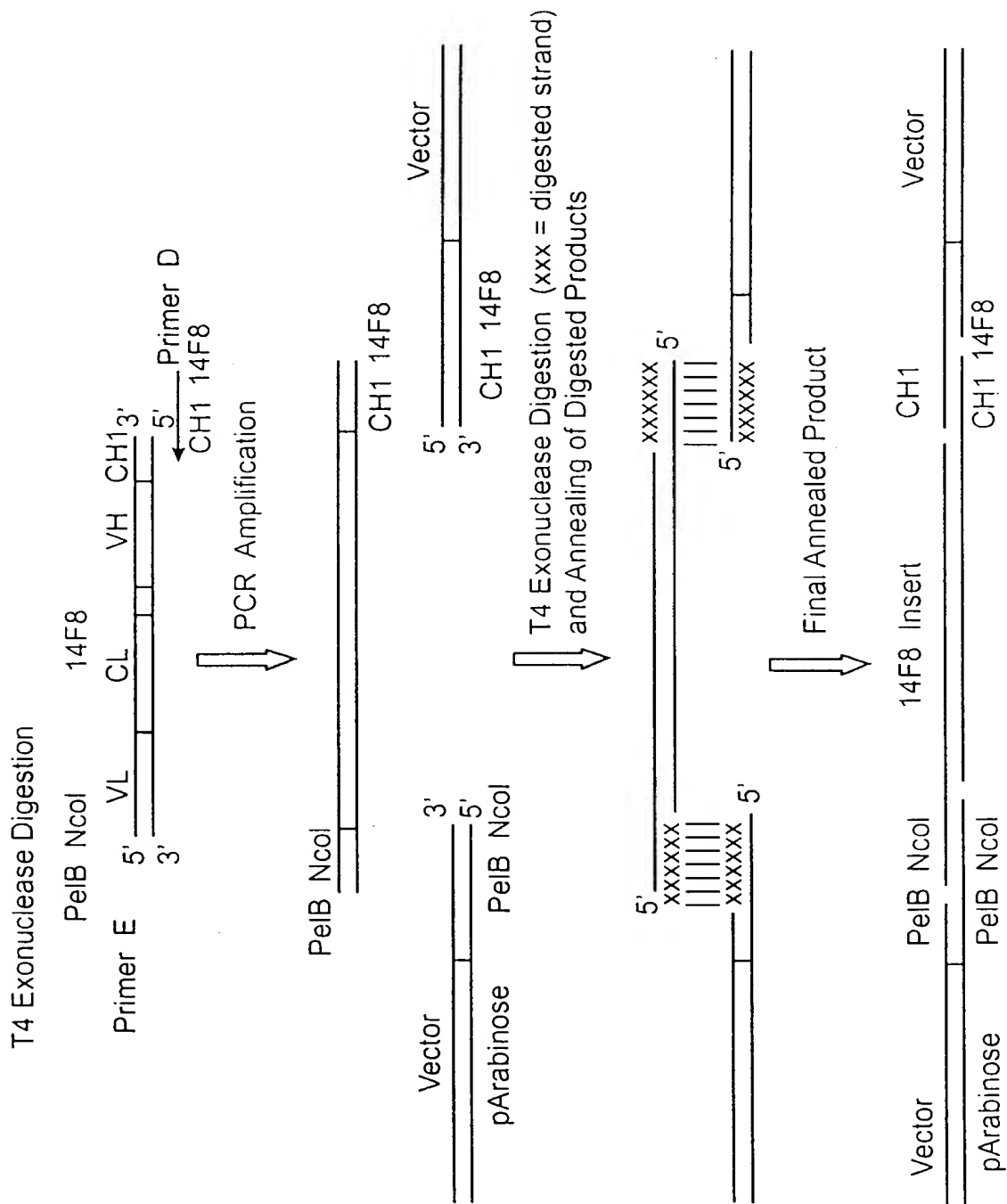


FIG. 5

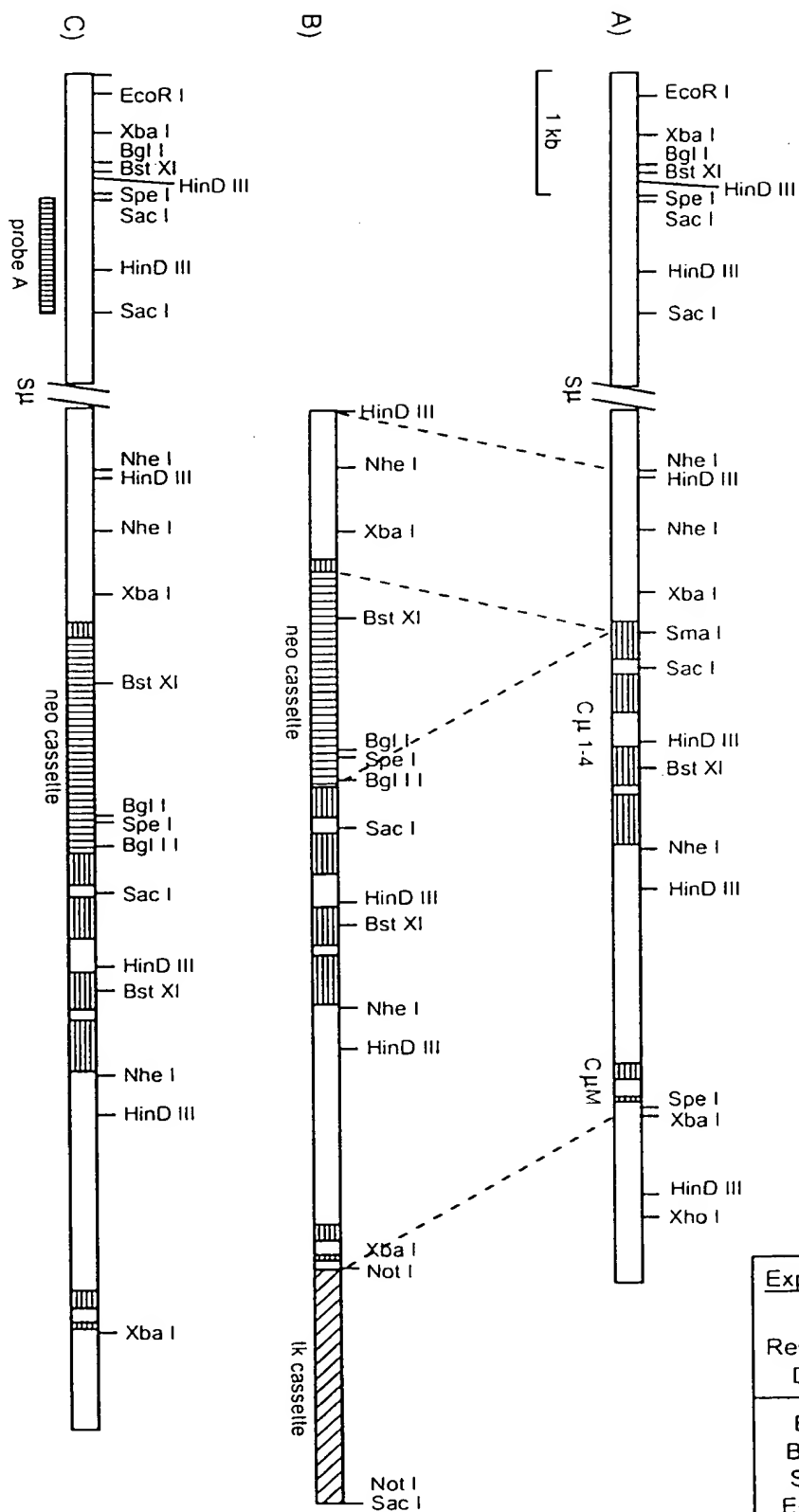


FIG. 6

| Expected Fragment Sizes (kb) using Probe A | | |
|---|-----------------|--------|
| Restriction Digest | Fragment Length | |
| | wild type | mutant |
| Bgl I | 15.7 | 7.7 |
| Bst XI | 7.3 | 6.6 |
| Spe I | 9.9 | 7.6 |
| Eco RI | 12.5 | 14.3 |

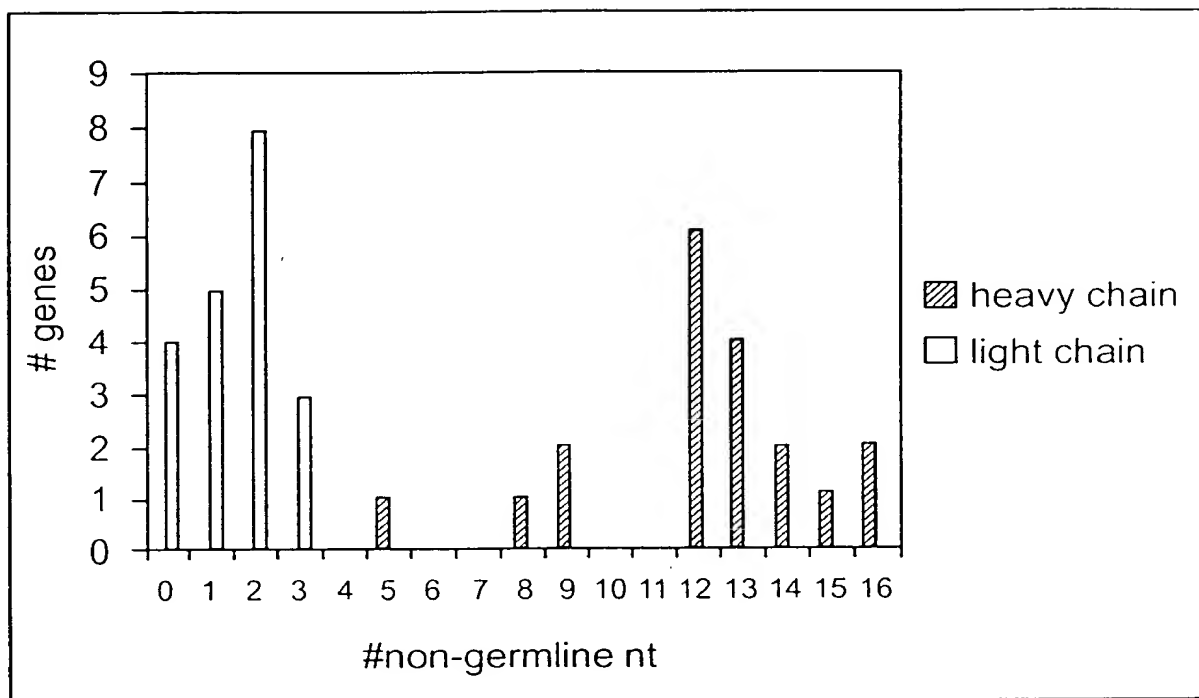


FIG. 7